

SEQUENCE LISTING

<110> Bennett, Michele
Brodbeck, Robbin
Krause, James

<120> Chimeric Neuropeptide Y Receptors

<130> N2000.001

<140> Not Yet Assigned
<141> 2000-01-28

<160> 31

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Homo sapiens

<400> 1

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<213> Homo sapiens

<400> 2

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Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly
35 40 45

Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile
50 55 60

Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val
65 70 75 80

Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu Pro Phe
85 90 95

Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met
100 105 110

Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile
115 120 125

Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn
130 135 140

Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly Ile Ala
145 150 155 160

Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr
165 170 175

Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr
180 185 190

Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg
195 200 205

Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu
210 215 220

Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
245 250 255

Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe
260 265 270

Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp
275 280 285

Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu
290 295 300

Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr
305 310 315 320
Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn
325 330 335
Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met
340 345 350
Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser
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Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile
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<213> Rattus norvegicus

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20 25 30

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35 40 45

Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile Ile
50 55 60

Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val Asn
65 70 75 80

Leu Ser Phe Ser Asp Leu Leu Val Ala Val Met Cys Leu Pro Phe Thr
85 90 95

Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Thr Met Cys
100 105 110

Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile Phe
115 120 125

Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn Pro
130 135 140

Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Ile Gly Ile Thr Val
145 150 155 160

Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Val Ile Tyr Gln

165	170	175	
Ile Leu Thr Asp Glu Pro Phe Gln Asn Val Ser Leu Ala Ala Phe Lys			
180	185	190	
Asp Lys Tyr Val Cys Phe Asp Lys Phe Pro Ser Asp Ser His Arg Leu			
195	200	205	
Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu Cys			
210	215	220	
Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg Arg			
225	230	235	240
Asn Asn Met Met Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Glu			
245	250	255	
Thr Lys Arg Ile Asn Val Met Leu Leu Ser Ile Val Val Ala Phe Ala			
260	265	270	
Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp Asn			
275	280	285	
His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu Cys			
290	295	300	
His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr Gly			
305	310	315	320
Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe			
325	330	335	
Cys Asp Phe Arg Ser Arg Asp Asp Tyr Glu Thr Ile Ala Met Ser			
340	345	350	
Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro			
355	360	365	
Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Ile			
370	375	380	

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 <213> Homo sapiens

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<211> 1069
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:Y5/Y1 CHIMERA

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<223> Description of Artificial Sequence:Y5/Y1 CHIMERA

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Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp
35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu
50 55 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser
85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val
100 105 110

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro
115 120 125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser
130 135 140

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn
145 150 155 160

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu
165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu
180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys
195 200 205

Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser
210 215 220

Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser
225 230 235 240

His Thr Ser Val Cys Ile Arg Leu Lys Arg Arg Asn Asn Met Met Asp
245 250 255

Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val Phe
260 265 270

Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro
275 280 285

Leu His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser
290 295 300

Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met
305 310 315 320

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu
165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu
180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys
195 200 205

Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser
210 215 220

Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser
225 230 235 240

His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser Asn Lys Glu
245 250 255

Asn Arg Leu Glu Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser
260 265 270

Lys Lys Ser Gly Pro Gln Val Lys Leu Ser Gly Ser His Lys Trp Ser
275 280 285

Tyr Ser Phe Ile Lys Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala
290 295 300

Cys Val Leu Pro Ala Pro Glu Arg Pro Ser Gln Glu Asn His Ser Arg
305 310 315 320

Ile Leu Pro Glu Asn Phe Gly Ser Val Arg Ser Gln Leu Ser Ser Ser
325 330 335

Ser Lys Phe Ile Pro Gly Val Pro Thr Cys Phe Glu Ile Lys Pro Glu
340 345 350

Glu Asn Ser Asp Val His Glu Leu Arg Val Lys Arg Ser Val Thr Arg
355 360 365

Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile
370 375 380

Leu Val Phe Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val
385 390 395 400

Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val
405 410 415

Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro
420 425 430

Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe
435 440 445

Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr
450 455 460

Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys
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Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn
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Glu Lys Ile

<210> 10

<211> 394

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Y5/Y1 CHIMERA

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Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp
35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu
50 55 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser
85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val
100 105 110

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro
115 120 125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser
130 135 140

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn
145 150 155 160

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu
165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu
180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys

195

200

205

Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser
210 215 220

Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser
225 230 235 240

His Thr Ser Val Cys Ile Arg Leu Lys Arg Arg Asn Asn Met Met Asp
245 250 255

Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val Phe
260 265 270

Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met Pro
275 280 285

Leu His Leu Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile Ser
290 295 300

Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly Met
305 310 315 320

Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly
325 330 335

Ile Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp Phe Arg Ser
340 345 350

Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His Thr Asp
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Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe Lys Lys
370 375 380

Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile
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<210> 11
<211> 6
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:HEXAHIStADiNE
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<400> 11
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<210> 12
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<220>

<223> Description of Artificial Sequence:FLAG EPITOPE
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<400> 12

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<210> 13

<211> 455

<212> PRT

<213> Homo sapiens

<400> 13

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Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr
20 25 30

Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp
35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu
50 55 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser
85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val
100 105 110

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro
115 120 125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser
130 135 140

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn
145 150 155 160

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu
165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu
180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys
195 200 205

Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser
210 215 220

Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser
225 230 235 240

His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser Asn Lys Glu
245 250 255

Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser
260 265 270

Lys Lys Ser Gly Pro Gln Val Lys Leu Ser Gly Ser His Lys Trp Ser
275 280 285

Tyr Ser Phe Ile Lys Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala
290 295 300

Cys Val Leu Pro Ala Pro Glu Arg Pro Ser Gln Glu Asn His Ser Arg
305 310 315 320

Ile Leu Pro Glu Asn Phe Gly Ser Val Arg Ser Gln Leu Ser Ser Ser
325 330 335

Ser Lys Phe Ile Pro Gly Val Pro Thr Cys Phe Glu Ile Lys Pro Glu
340 345 350

Glu Asn Ser Asp Val His Glu Leu Arg Val Lys Arg Ser Val Thr Arg
355 360 365

Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile
370 375 380

Leu Val Phe Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val
385 390 395 400

Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val
405 410 415

Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro
420 425 430

Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Val Ser
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Leu Ile His Cys Leu His Met
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<210> 14
<211> 21
<212> DNA
<213> Homo sapiens

<400> 14
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<210> 15

<211> 26
<212> DNA
<213> Homo sapiens

<400> 15
ccttggtaaa cagtgagaat tattac 26

<210> 16
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CHIMERIC Y1/Y5
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<400> 16
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gta 63

<210> 17
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CHIMERIC Y1/Y5
PRIMER

<400> 17
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aggcgtatgc a 71

<210> 18
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MUTAGENIC R1
PRIMER

<400> 18
gaacaaaaga attcagagag acttgcagtt c 31

<210> 19
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MUTAGENIC R1
PRIMER

<400> 19

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28

<210> 20

<211> 341

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

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Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val Trp Asp Asp
20 25 30

Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr
35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met
50 55 60

Ala Leu Met Arg Lys Arg Asn Gln Lys Thr Met Val Asn Phe Leu Ile
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro
85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val
100 105 110

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser
115 120 125

Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys
130 135 140

His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile
145 150 155 160

Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val
165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Asp Ser Ala Leu Leu
180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg
195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Val Gln Tyr Ile Leu Pro Leu
210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg

225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
245 250 255

Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe
260 265 270

Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe
275 280 285

Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile
290 295 300

Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr
305 310 315 320

Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Ile Ser Leu Ile Gln
325 330 335

Cys Leu His Met Ser
340

<210> 21
<211> 383
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Y1/Y5 CHIMERA

<400> 21
Met Asp Leu Glu Leu Gln Asp Phe Tyr Asn Lys Thr Leu Ala Thr Glu
1 5 10 15

Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val Trp Asp Asp
20 25 30

Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr
35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met
50 55 60

Ala Leu Met Arg Lys Arg Asn Gln Lys Thr Met Val Asn Phe Leu Ile
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro
85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val
100 105 110

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser
115 120 125

Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn Gly
325 330 335

Ile Lys Ala Asp Leu Val Ser Leu Ile His Cys Leu His Met
340 345 350

<210> 7
<211> 1500
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Y5/Y1 CHIMERA

<400> 7
atgtttttt attccaagca ggactataat atggat tag agctcgacga gtattataac 60
aagacacttg ccacagagaa taatactgct gccactcgga attctgattt cccagtctgg 120
gatgactata aaagoagtgt agatgactta cagtatttc tgattggctt ctatacattt 180
gtaagtcttc ttggctttat gggaatcta cttatattaa tggctctcat gaaaaagcgt 240
aatcagaaga ctacgtaaaa cttcctcata ggcaatctgg cttttctga tatctgggtt 300
gtgctgtttt gtcacacccctt cacaactgacg tctgtctgc tggatcagtg gatgtttggc 360
aaagtcatgt gccatattat gccttttctt caatgtgtt cagttttggt ttcaacttta 420
attttaatat caatttccat tggctcaggat catatgataaa aacatcccat atctaataat 480
ttaacagcaa accatggcta ctttctgata gctactgtct ggacacttagg ttttgcacatc 540
tggctccccc ttccagtggtt tcacagtctt gtggaaacttc aagaaaacattt tggttcagca 600
ttgctgagca gcaggattttt atgtgtttag tcattggccat ctgattcata cagaatttgc 660
tttactatct ctttattgtt agttcagttt atctgcctt tagtttgcct tactgttaagt 720
catacaagtg tctgcagaag tataagctgtt ggatttgcca acaaagaaaaa cagacttgaa 780
gaaaatgaga tggatcaactt aactcttcat ccatccaaaa agagttggcc tcaggtgaaa 840
ctctctggca gccataaaatg gagttattca ttcatccaaaa aacacagaag aagatatagc 900
aagaagacag catgtgtgtt acctgctcca gaaagacctt ctcaagagaa ccactccaga 960
atacttccag aaaactttgg ctctgttata agtcaacttctt cttcatccag taagttcata 1020
ccagggttcc ccacttgctt tgagataaaa cctgaagaaa attcagatgt tcattttttt 1080
agagtaaaaac gttctgttac aagaataaaa aagagatctc gaagttttt ctacagactg 1140
accataactga tattttttt tgctgttagt tggatgcccac tacaccctttt ccatgtggta 1200
actgattttt atgacaatct tattttcaat aggcatatca agttgggtta ttgcattttgt 1260
cattttttgg gcatgtatgtc ctgtttgtt aatccaaattc tatatgggtt tcttaataat 1320
gaaattcaga gagacttgca gttcttctt aacttttggt atttccggc tcgggatgat 1380
gattatgaaa caatagccat gtccacgatg cacacagatg tttccaaaac ttcttgaag 1440
caagcaagcc cagtcgcatt taaaaaaaatc aacaacaatg atgataatga aaaaatctga 1500

<210> 8
<211> 1201
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Y5/Y1 CHIMERA

<400> 8
ttttgggttgc tgacaaatgt ctttttatttca agcaggac tataatatgg atttagagct 60
cgacgagtttataacaaga cacttgccac agagaataat actgctgcca ctcggaaattc 120
tgattttccca gtctggatg actataaaaag cagtgttagat gacttacagt attttctgtat 180
tgggctctat acatttggtaa gtcttcttgg ctttatgggg aatctactta tttaatggc 240

Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys
130 135 140

His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile
145 150 155 160

Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val
165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Asp Ser Ala Leu Leu
180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg
195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu
210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg
225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
245 250 255

Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe
260 265 270

Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe
275 280 285

Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile
290 295 300

Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr
305 310 315 320

Gly Phe Leu Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe Phe Asn
325 330 335

Phe Cys Asp Phe Arg Ser Arg Asp Asp Tyr Glu Thr Ile Ala Met
340 345 350

Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser
355 360 365

Pro Val Ala Phe Lys Lys Ile Asn Asn Asp Asp Asn Glu Lys Ile
370 375 380

<210> 22
<211> 508
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 22

Met	Glu	Val	Lys	Leu	Glu	Glu	His	Phe	Asn	Lys	Thr	Phe	Val	Thr	Glu
1				5				10						15	
Asn	Asn	Thr	Ala	Ala	Ser	Gln	Asn	Thr	Ala	Ser	Pro	Ala	Trp	Glu	Asp
			20					25					30		
Tyr	Arg	Gly	Thr	Glu	Asn	Asn	Thr	Ser	Ala	Ala	Arg	Asn	Thr	Ala	Phe
		35						40					45		
Pro	Val	Trp	Glu	Asp	Tyr	Arg	Gly	Ser	Val	Asp	Asp	Leu	Gln	Tyr	Phe
	50				55					60					
Leu	Ile	Gly	Leu	Tyr	Thr	Phe	Val	Ser	Leu	Leu	Gly	Phe	Met	Gly	Asn
	65				70				75				80		
Leu	Leu	Ile	Leu	Met	Ala	Val	Met	Lys	Lys	Arg	Asn	Gln	Lys	Thr	Thr
			85					90					95		
Val	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Phe	Ser	Asp	Ile	Leu	Val	Val
		100					105					110			
Leu	Phe	Cys	Ser	Pro	Phe	Thr	Leu	Thr	Ser	Val	Leu	Leu	Asp	Gln	Trp
		115				120					125				
Met	Phe	Gly	Lys	Ala	Met	Cys	His	Ile	Met	Pro	Phe	Leu	Gln	Cys	Val
		130				135					140				
Ser	Val	Leu	Val	Ser	Thr	Leu	Ile	Leu	Ile	Ser	Ile	Ala	Ile	Val	Arg
	145				150				155				160		
Tyr	His	Met	Ile	Lys	His	Pro	Ile	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His
			165				170					175			
Gly	Tyr	Phe	Leu	Ile	Ala	Thr	Val	Trp	Thr	Leu	Gly	Phe	Ala	Ile	Cys
		180				185					190				
Ser	Pro	Phe	Pro	Val	Phe	His	Ser	Leu	Val	Glu	Leu	Lys	Glu	Thr	Phe
		195				200				205					
Gly	Ser	Ala	Leu	Leu	Ser	Ser	Lys	Tyr	Leu	Cys	Val	Glu	Ser	Trp	Pro
		210				215				220					
Ser	Asp	Ser	Tyr	Arg	Ile	Ala	Phe	Thr	Ile	Ser	Leu	Leu	Leu	Val	Gln
	225				230				235				240		
Tyr	Ile	Leu	Pro	Leu	Val	Cys	Leu	Thr	Val	Ser	His	Thr	Ser	Val	Cys
			245			250					255				
Arg	Ser	Ile	Ser	Cys	Gly	Leu	Ser	His	Lys	Glu	Asn	Arg	Leu	Glu	Glu
			260				265				270				
Asn	Glu	Met	Ile	Asn	Leu	Thr	Leu	His	Pro	Ser	Lys	Lys	Ser	Arg	Asp
			275			280					285				
Gln	Ala	Lys	Pro	Pro	Ser	Thr	Gln	Lys	Trp	Ser	Tyr	Ser	Phe	Ile	Arg
		290				295				300					

Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala
305 310 315 320

Pro Ala Gly Pro Ser Gln Glu Lys His Leu Thr Val Pro Glu Asn Pro
325 330 335

Gly Ser Val Arg Ser Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly
340 345 350

Val Pro Ile Cys Phe Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln
355 360 365

Glu Met Arg Val Lys Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg
370 375 380

Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser
385 390 395 400

Trp Met Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn
405 410 415

Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu
420 425 430

Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu
435 440 445

Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp
450 455 460

Phe Arg Ser Arg Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met
465 470 475 480

His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala
485 490 495

Phe Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Val
500 505

<210> 23

<211> 352

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 23

Met Asp Val Leu Phe Phe His Gln Asp Ser Ser Met Glu Phe Lys Leu
1 5 10 15

Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala
20 25 30

Ala Arg Asn Ala Ala Phe Pro Ala Trp Glu Asp Tyr Arg Gly Ser Val

35

40

45

Asp	Asp	Leu	Gln	Tyr	Phe	Leu	Ile	Gly	Leu	Tyr	Thr	Phe	Val	Ser	Leu
50					55					60					
Leu	Gly	Phe	Met	Gly	Asn	Leu	Leu	Ile	Leu	Met	Ala	Val	Met	Lys	Lys
65					70					75				80	
Arg	Asn	Gln	Lys	Thr	Thr	Val	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Phe
				85			90					95			
Ser	Asp	Ile	Leu	Val	Val	Leu	Phe	Cys	Ser	Pro	Phe	Thr	Leu	Thr	Ser
				100			105				110				
Val	Leu	Leu	Asp	Gln	Trp	Met	Phe	Gly	Lys	Ala	Met	Cys	His	Ile	Met
				115			120				125				
Pro	Phe	Leu	Gln	Cys	Val	Ser	Val	Leu	Val	Ser	Thr	Leu	Ile	Leu	Ile
				130			135				140				
Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys	His	Pro	Ile	Ser	Asn
				145			150				155			160	
Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	Ala	Thr	Val	Trp	Thr
				165			170				175				
Leu	Gly	Phe	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	Phe	His	Ser	Leu	Val
				180			185				190				
Glu	Leu	Lys	Glu	Thr	Phe	Gly	Ser	Ala	Leu	Leu	Ser	Ser	Lys	Tyr	Leu
				195			200				205				
Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	Ile	Ala	Phe	Thr	Ile
				210			215				220				
Ser	Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	Val	Cys	Leu	Thr	Val
				225			230				235			240	
Ser	His	Thr	Ser	Val	Cys	Ile	Arg	Leu	Lys	Arg	Arg	Asn	Asn	Met	Met
				245			250				255				
Asp	Lys	Ile	Arg	Asp	Ser	Lys	Tyr	Arg	Ser	Ser	Arg	Ser	Arg	Ser	Val
				260			265				270				
Phe	Tyr	Arg	Leu	Thr	Ile	Leu	Ile	Leu	Val	Phe	Ala	Val	Ser	Trp	Met
				275			280				285				
Pro	Leu	His	Val	Phe	His	Val	Val	Thr	Asp	Phe	Asn	Asp	Asn	Leu	Ile
				290			295				300				
Ser	Asn	Arg	His	Phe	Lys	Leu	Val	Tyr	Cys	Ile	Cys	His	Leu	Leu	Gly
				305			310				315			320	
Met	Met	Ser	Cys	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	Gly	Phe	Leu	Asn	Asn
				325			330				335				
Gly	Ile	Lys	Ala	Asp	Leu	Arg	Ala	Leu	Ile	His	Cys	Leu	His	Met	Ser

340

345

350

<210> 24

<211> 499

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Y1/Y5 CHIMERA

<400> 24

Met	Asp	Val	Leu	Phe	Phe	His	Gln	Asp	Ser	Ser	Met	Glu	Phe	Lys	Leu
1				5					10					15	
Glu	Glu	His	Phe	Asn	Lys	Thr	Phe	Val	Thr	Glu	Asn	Asn	Thr	Ala	Ala
				20				25					30		
Ala	Arg	Asn	Ala	Ala	Phe	Pro	Ala	Trp	Glu	Asp	Tyr	Arg	Gly	Ser	Val
					35				40			45			
Asp	Asp	Leu	Gln	Tyr	Phe	Leu	Ile	Gly	Leu	Tyr	Thr	Phe	Val	Ser	Leu
				50		55				60					
Leu	Gly	Phe	Met	Gly	Asn	Leu	Leu	Ile	Leu	Met	Ala	Val	Met	Lys	Lys
			65		70				75				80		
Arg	Asn	Gln	Lys	Thr	Thr	Val	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Phe
				85				90				95			
Ser	Asp	Ile	Leu	Val	Val	Leu	Phe	Cys	Ser	Pro	Phe	Thr	Leu	Thr	Ser
				100				105				110			
Val	Leu	Leu	Asp	Gln	Trp	Met	Phe	Gly	Lys	Ala	Met	Cys	His	Ile	Met
				115			120				125				
Pro	Phe	Leu	Gln	Cys	Val	Ser	Val	Leu	Val	Ser	Thr	Leu	Ile	Leu	Ile
				130		135				140					
Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys	His	Pro	Ile	Ser	Asn
				145		150				155			160		
Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	Ala	Thr	Val	Trp	Thr
				165				170				175			
Leu	Gly	Phe	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	Phe	His	Ser	Leu	Val
				180				185				190			
Glu	Leu	Lys	Glu	Thr	Phe	Gly	Ser	Ala	Leu	Leu	Ser	Ser	Lys	Tyr	Leu
				195			200				205				
Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	Ile	Ala	Phe	Thr	Ile
				210		215				220					

Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val
225 230 235 240

Ser His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser His Lys
245 250 255

Glu Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu Gln Pro
260 265 270

Ser Lys Lys Ser Arg Asn Gln Ala Lys Thr Pro Ser Thr Gln Lys Trp
275 280 285

Ser Tyr Ser Phe Ile Arg Lys His Arg Arg Arg Tyr Ser Lys Lys Thr
290 295 300

Ala Cys Val Leu Pro Ala Pro Ala Gly Pro Ser Gln Gly Lys His Leu
305 310 315 320

Ala Val Pro Glu Asn Pro Ala Ser Val Arg Ser Gln Leu Ser Pro Ser
325 330 335

Ser Lys Val Ile Pro Gly Val Pro Ile Cys Phe Glu Val Lys Pro Glu
340 345 350

Glu Ser Ser Asp Ala His Glu Met Arg Val Lys Arg Ser Ile Thr Arg
355 360 365

Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile
370 375 380

Leu Val Phe Ala Val Ser Trp Met Pro Leu His Val Phe His Val Val
385 390 395 400

Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val
405 410 415

Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro
420 425 430

Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys Gln Arg Asp Leu Gln
435 440 445

Phe Phe Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu
450 455 460

Thr Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu
465 470 475 480

Lys Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Ser Met Asn Asp Asn
485 490 495

Glu Lys Ile

<210> 25
<211> 395

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Y1/Y5 CHIMERA

<400> 25

Met Asp Val Leu Phe Phe His Gln Asp Ser Ser Met Glu Phe Lys Leu

1

5

10

15

Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala
20 25 30

Ala Arg Asn Ala Ala Phe Pro Ala Trp Glu Asp Tyr Arg Gly Ser Val
35 40 45

Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu
50 55 60

Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Val Met Lys Lys
65 70 75 80

Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe
85 90 95

Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser
100 105 110

Val Leu Leu Asp Gln Trp Met Phe Gly Lys Ala Met Cys His Ile Met
115 120 125

Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile
130 135 140

Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn
145 150 155 160

Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr
165 170 175

Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val
180 185 190

Glu Leu Lys Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Lys Tyr Leu
195 200 205

Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile
210 215 220

Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val
225 230 235 240

Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg Arg Asn Asn Met Met
245 250 255

Asp Lys Ile Arg Asp Ser Lys Tyr Arg Ser Ser Arg Ser Arg Ser Val
260 265 270

Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met
275 280 285

Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile
290 295 300

Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly
305 310 315 320

Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn
325 330 335

Gly Ile Lys Gln Arg Asp Leu Gln Phe Phe Asn Phe Cys Asp Phe
340 345 350

Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His
355 360 365

Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe
370 375 380

Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Ile
385 390 395

<210> 26
<211> 341
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Y1/Y5 CHIMERA

<400> 26
Met Gly Ser Glu Ile Pro Asp Tyr Tyr Asn Lys Thr Leu Ala Ser Glu
1 5 10 15

Asn Asn Thr Val Ala Thr Arg Asn Ser Gly Phe Pro Val Trp Glu Asp
20 25 30

Tyr Lys Gly Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr
35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met
50 55 60

Ala Val Met Arg Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro
85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val
100 105 110

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Thr Val Leu Val Ser

115	120	125
Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys		
130	135	140
His Pro Val Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile		
145	150	155
Ala Thr Val Trp Thr Leu Gly Leu Ala Ile Cys Ser Pro Leu Pro Val		
165	170	175
Phe His Ser Leu Val Glu Leu Gln Glu Ser Phe Gly Ser Ala Trp Leu		
180	185	190
Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg		
195	200	205
Ile Ala Phe Thr Ile Ser Leu Leu Val Gln Tyr Ile Leu Pro Leu		
210	215	220
Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg		
225	230	235
Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser		
245	250	255
Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Val Leu Ile Leu Val Phe		
260	265	270
Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe		
275	280	285
Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile		
290	295	300
Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr		
305	310	315
Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Met Ser Leu Ile His		
325	330	335
Cys Leu His Val Ser		
340		

<210> 27
 <211> 383
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 27
 Met Gly Ser Glu Ile Pro Asp Tyr Tyr Asn Lys Thr Leu Ala Ser Glu
 1 5 10 15

Asn Asn Thr Val Ala Thr Arg Asn Ser Gly Phe Pro Val Trp Glu Asp
20 25 30

Tyr Lys Gly Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr
35 40 45

Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met
50 55 60

Ala Val Met Arg Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile
65 70 75 80

Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro
85 90 95

Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val
100 105 110

Met Cys His Ile Met Pro Phe Leu Gln Cys Val Thr Val Leu Val Ser
115 120 125

Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys
130 135 140

His Pro Val Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile
145 150 155 160

Ala Thr Val Trp Thr Leu Gly Leu Ala Ile Cys Ser Pro Leu Pro Val
165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Ser Phe Gly Ser Ala Trp Leu
180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg
195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu
210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg
225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
245 250 255

Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Val Leu Ile Leu Val Phe
260 265 270

Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe
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Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr
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Phe Cys Asp Phe Arg Ser Arg Asp Asp Tyr Glu Val Ile Ala Met
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Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu
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His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser Asn Lys Glu
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Arg Lys Ile Gly Pro Gln Val Lys Leu Ser Gly Ser His Lys Trp Ser
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Tyr Ser Phe Ile Lys Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala
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Cys Val Leu Pro Ala Pro Glu Arg Pro Ser Gln Glu Asn His Ser Arg
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Ile Leu Pro Glu Asn Phe Gly Ser Val Arg Ser Gln Leu Ser Ser Ser
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Ser Lys Phe Ile Pro Gly Val Pro Thr Cys Phe Glu Ile Lys Pro Glu
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Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile
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Leu Val Phe Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val
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Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val
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Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro
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